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RAW SEQUENCE LISTING                    DATE: 01/25/2002
PATENT APPLICATION:  US/09/898,216      TIME: 16:58:04

Input Set : N:\Crf3\RULE60\09898216.raw
Output Set: N:\CRF3\01252002\I898216.raw

**SEQUENCE LISTING**
```
 3 (1) GENERAL INFORMATION:
 5       (i) APPLICANT: Hillman, Jennifer L.
 6                      Goli, Surya K.
 8      (ii) TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN
10     (iii) NUMBER OF SEQUENCES: 7
12      (iv) CORRESPONDENCE ADDRESS:
13           (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
14           (B) STREET: 3174 Porter Drive
15           (C) CITY: Palo Alto
16           (D) STATE: CA
17           (E) COUNTRY: USA
18           (F) ZIP: 94304
20       (v) COMPUTER READABLE FORM:
21           (A) MEDIUM TYPE: Diskette
22           (B) COMPUTER: IBM Compatible
23           (C) OPERATING SYSTEM: DOS
24           (D) SOFTWARE: FastSEQ for Windows Version 2.0
26      (vi) CURRENT APPLICATION DATA:
27           (A) APPLICATION NUMBER: US/09/898,216
28           (B) FILING DATE: 02-Jul-2001
29           (C) CLASSIFICATION:
31     (vii) PRIOR APPLICATION DATA:
32           (A) APPLICATION NUMBER: 08/781,562
33           (B) FILING DATE:
35    (viii) ATTORNEY/AGENT INFORMATION:
36           (A) NAME: Billings, Lucy J.
37           (B) REGISTRATION NUMBER: 36,749
38           (C) REFERENCE/DOCKET NUMBER: PF-0181 US
40      (ix) TELECOMMUNICATION INFORMATION:
41           (A) TELEPHONE: 415-855-0555
42           (B) TELEFAX: 415-845-4166
43           (C) TELEX:
46 (2) INFORMATION FOR SEQ ID NO: 1:
48       (i) SEQUENCE CHARACTERISTICS:
49           (A) LENGTH: 356 amino acids
50           (B) TYPE: amino acid
51           (C) STRANDEDNESS: single
52           (D) TOPOLOGY: linear
54     (vii) IMMEDIATE SOURCE:
55           (A) LIBRARY: Consensus
56           (B) CLONE: Consensus
58      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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C--> 27
C--> 28

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```
    60  Met Leu Ala Arg Ala Ala Arg Gly His Trp Gly Pro Phe Ala Glu Gly
    61   1                   5                  10                  15
    62  Leu Ser Thr Gly Phe Trp Pro Arg Ser Gly Arg Ala Ser Ser Gly Leu
    63                  20                  25                  30
    64  Pro Arg Asn Thr Val Val Leu Phe Val Pro Gln Gln Glu Ala Trp Val
    65              35                  40                  45
    66  Val Glu Arg Met Gly Arg Phe His Arg Ile Leu Glu Pro Gly Leu Asn
    67      50                  55                  60
    68  Ile Leu Ile Pro Val Leu Asp Arg Ile Arg Tyr Val Gln Ser Leu Lys
    69  65                  70                  75                  80
    70  Glu Ile Val Ile Asn Val Pro Glu Gln Ser Ala Val Thr Leu Asp Asn
    71                  85                  90                  95
    72  Val Thr Leu Gln Ile Asp Gly Val Leu Tyr Leu Arg Ile Met Asp Pro
    73              100                 105                 110
    74  Tyr Lys Ala Ser Tyr Gly Val Glu Asp Pro Glu Tyr Ala Val Thr Gln
    75          115                 120                 125
W--> 76  Leu Ala Gln Thr Thr Met Arg Ser Glu Leu Gly Lys Leu Ser Xaa Asp
    77          130                 135                 140
    78  Lys Val Phe Arg Glu Arg Glu Ser Leu Asn Ala Ser Ile Val Asp Ala
    79  145                 150                 155                 160
    80  Ile Asn Gln Ala Ala Asp Cys Trp Gly Ile Arg Cys Leu Arg Tyr Glu
    81              165                 170                 175
    82  Ile Lys Asp Ile His Val Pro Pro Arg Val Lys Glu Ser Met Gln Met
    83              180                 185                 190
    84  Gln Val Glu Ala Glu Arg Arg Lys Arg Ala Thr Val Leu Glu Ser Glu
    85          195                 200                 205
    86  Gly Thr Arg Glu Ser Ala Ile Asn Val Ala Glu Gly Lys Lys Gln Ala
    87          210                 215                 220
    88  Gln Ile Leu Ala Ser Glu Ala Glu Lys Ala Glu Gln Ile Asn Gln Ala
    89  225                 230                 235                 240
    90  Ala Gly Glu Ala Ser Ala Val Leu Ala Lys Ala Lys Ala Lys Ala Glu
    91                  245                 250                 255
    92  Ala Ile Arg Ile Leu Ala Ala Ala Leu Thr Gln His Asn Gly Asp Ala
    93              260                 265                 270
    94  Ala Ala Ser Leu Thr Val Ala Glu Gln Tyr Val Ser Ala Phe Ser Lys
    95          275                 280                 285
    96  Leu Ala Lys Asp Ser Asn Thr Ile Leu Leu Pro Ser Asn Pro Gly Asp
    97          290                 295                 300
    98  Val Thr Ser Met Val Ala Gln Ala Met Gly Val Tyr Gly Ala Leu Thr
    99  305                 310                 315                 320
   100  Lys Ala Pro Val Pro Gly Thr Pro Asp Ser Leu Ser Ser Gly Ser Ser
   101                  325                 330                 335
W--> 102 Arg Asp Val Gln Gly Thr Asp Ala Ser Xaa Asp Glu Glu Leu Asp Arg
   103              340                 345                 350
   104  Val Lys Met Ser
   105              355
```

107 (2) INFORMATION FOR SEQ ID NO: 2:
109      (i) SEQUENCE CHARACTERISTICS:
110          (A) LENGTH: 1188 base pairs

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Input Set : N:\Crf3\RULE60\09898216.raw
Output Set: N:\CRF3\01252002\I898216.raw

```
111          (B) TYPE: nucleic acid
112          (C) STRANDEDNESS: single
113          (D) TOPOLOGY: linear
115     (vii) IMMEDIATE SOURCE:
116          (A) LIBRARY: Consensus
117          (B) CLONE: Consensus
119     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
121  GGCTTCTGGG AGCNACCGCT CCGCTCGTCT CGTTGGTTCC GGAGGTCGCT GCGGCGGTGG    60
122  GAAATGCTGG CGCGCGCGGC GCGGGGGCAC TGGGGCCCTT TTGCTGAGGG GCTCTCTACT   120
123  GGCTTCTGGC CGCGCTCCGG CCGCGCCTCC TCTGGATTGC CCCGAAACAC CGTGGTACTG   180
124  TTCGTGCCGC AGCAGGAGGC CTGGGTGGTG GAGCGAATGG GCCGATTCCA CCGGATCCTG   240
125  GAGCCTGGTT TGAACATCCT CATCCCTGTG TTAGACCGGA TCCGATATGT GCAGAGTCTC   300
126  AAGGAAATTG TCATCAACGT GCCTGAGCAG TCGGCTGTGA CTCTCGACAA TGTAACTCTG   360
127  CAAATCGATG GAGTCCTTTA CCTGCGCATC ATGGACCCTT ACAAGGCAAG CTACGGTGTG   420
128  GAGGACCCTG AGTATGCCGT CACCCAGCTA GCTCAAACAA CCATGAGATC AGAGCTCGGC   480
129  AAACTCTCTN TGGACAAAGT CTTCCGGGAA CGGGAGTCCC TGAATGCCAG CATTGTGGAT   540
130  GCCATCAACC AAGCTGCTGA CTGCTGGGGT ATCCGCTGCC TNCGTTATGA GATCAAGGAT   600
131  ATCCATGTGC CACCCCGGGT GAAAGAGTCT ATGCAGATGC AGGTGGAGGC AGAGCGGCGG   660
132  AAACGGGCCA CAGTTCTAGA GTCTGAGGGG ACCCGAGAGT CGGCCATCAA TGTGGCAGAA   720
133  GGGAAGAAAC AGGCCCAGAT CCTGGCCTCC GAAGCAGAAA AGGCTGAACA GATAAATCAG   780
134  GCAGCAGGAG AGGCCAGTGC AGTTCTGGCG AAGGCCAAGG CTAAAGCTGA AGCTATTCGA   840
135  ATCCTGGCTG CAGCTCTGAC ACAACATAAT GGAGATGCAG CAGCTTCACT GACTGTGGCC   900
136  GAGCAGTATG TCAGCGCGTT CTCCAAACTG GCCAAGGACT CCAACACTAT CCTACTGCCC   960
137  TCCAACCCTG GCGATGTCAC CAGCATGGTG GCTCAGGCCA TGGGTGTATA TGGAGCCCTC  1020
138  ACCAAAGCCC CAGTGCCAGG GACTCCAGAC TCACTCTCCA GTGGGAGCAG CAGAGATGTC  1080
139  CAGGGTACAG ATGCAAGTNT TGATGAGGAA CTTGATCGAG TCAAGATGAG TTAGTGGAGC  1140
140  TGGGCTTNGC CAGGGAGTCT GGGGACAAGG AAGCAGATTT TCCTGATT           1188
142  (2) INFORMATION FOR SEQ ID NO: 3:
144       (i) SEQUENCE CHARACTERISTICS:
145          (A) LENGTH: 288 amino acids
146          (B) TYPE: amino acid
147          (C) STRANDEDNESS: single
148          (D) TOPOLOGY: linear
150      (vii) IMMEDIATE SOURCE:
151          (A) LIBRARY: Genbank
152          (B) CLONE: 31069
154     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
156  Met Ala Glu Lys Arg His Thr Arg Asp Ser Glu Ala Gln Arg Leu Pro
157   1           5                  10                  15
158  Asp Ser Phe Lys Asp Ser Pro Ser Lys Gly Leu Gly Pro Cys Gly Trp
159           20                  25                  30
160  Ile Leu Val Ala Phe Ser Phe Leu Phe Thr Val Ile Thr Phe Pro Ile
161           35                  40                  45
162  Ser Ile Trp Met Cys Ile Lys Ile Ile Lys Glu Tyr Glu Arg Ala Ile
163       50                  55                  60
164  Ile Phe Arg Leu Gly Arg Ile Leu Gln Gly Gly Ala Lys Gly Pro Gly
165  65                  70                  75                  80
166  Leu Phe Phe Ile Leu Pro Cys Thr Asp Ser Phe Ile Lys Val Asp Met
167               85                  90                  95
```

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DATE: 01/25/2002
TIME: 16:58:04

Input Set : N:\Crf3\RULE60\09898216.raw
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```
168  Arg Thr Ile Ser Phe Asp Ile Pro Pro Gln Glu Ile Leu Thr Lys Asp
169              100             105                 110
170  Ser Val Thr Ile Ser Val Asp Gly Val Val Tyr Tyr Arg Val Gln Asn
171              115             120                 125
172  Ala Thr Leu Ala Val Ala Asn Ile Thr Asn Ala Asp Ser Ala Thr Arg
173      130             135                 140
174  Leu Leu Ala Gln Thr Thr Leu Arg Asn Val Leu Gly Thr Lys Asn Leu
175  145             150                 155                 160
176  Ser Gln Ile Leu Ser Asp Arg Glu Glu Ile Ala His Asn Met Gln Ser
177              165                 170                 175
178  Thr Leu Asp Asp Ala Thr Asp Ala Trp Gly Ile Lys Val Glu Arg Val
179              180                 185                 190
180  Glu Ile Lys Asp Val Lys Leu Pro Val Gln Leu Gln Arg Ala Met Ala
181              195             200                 205
182  Ala Glu Ala Glu Ala Ser Arg Glu Ala Arg Ala Lys Val Ile Ala Ala
183      210             215                 220
184  Glu Gly Glu Met Asn Ala Ser Arg Ala Leu Lys Glu Ala Ser Met Val
185  225             230                 235                 240
186  Ile Thr Glu Ser Pro Ala Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu
187              245                 250                 255
188  Thr Thr Ile Ala Ala Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro
189              260                 265                 270
190  Ile Asp Met Leu Gln Gly Ile Ile Gly Ala Lys His Ser His Leu Gly
191              275                 280                 285
193  (2) INFORMATION FOR SEQ ID NO: 4:
195       (i) SEQUENCE CHARACTERISTICS:
196           (A) LENGTH: 280 amino acids
197           (B) TYPE: amino acid
198           (C) STRANDEDNESS: single
199           (D) TOPOLOGY: linear
201      (vii) IMMEDIATE SOURCE:
202           (A) LIBRARY: GenBank
203           (B) CLONE: 1065452
205      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
207  Met Asn Leu Lys Thr Cys Ser Leu Ser Thr His Ser Phe Leu Gln Lys
208  1               5                   10                  15
209  Lys Asn Glu Lys His Asp Gly Asn Pro Glu His Tyr Asp Thr Gly Leu
210              20                  25                  30
211  Gly Phe Cys Gly Trp Phe Leu Met Gly Leu Ser Trp Ile Met Val Ile
212      35                  40                  45
213  Ser Thr Phe Pro Val Ser Ile Tyr Phe Cys Met Lys Val Val Gln Glu
214      50                  55                  60
215  Tyr Glu Arg Ala Val Ile Phe Arg Leu Gly Arg Leu Ile Gly Gly Gly
216  65                  70                  75                  80
217  Ala Lys Gly Pro Gly Ile Phe Phe Val Leu Pro Cys Ile Glu Ser Tyr
218              85                  90                  95
219  Thr Lys Val Asp Leu Arg Thr Val Ser Phe Ser Val Pro Pro Gln Glu
220              100                 105                 110
221  Ile Leu Thr Lys Asp Ser Val Thr Thr Ser Val Asp Ala Val Ile Tyr
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PATENT APPLICATION: US/09/898,216    TIME: 16:58:04

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Input Set : N:\Crf3\RULE60\09898216.raw
Output Set: N:\CRF3\01252002\I898216.raw

222           115                 120                 125
223  Tyr Arg Ile Ser Asn Ala Thr Val Ser Val Ala Asn Val Glu Asn Ala
224       130                 135                 140
225  His His Ser Thr Arg Leu Leu Ala Gln Thr Thr Leu Arg Asn Met Leu
226  145                 150                 155                 160
227  Gly Thr Arg Ser Leu Ser Glu Ile Leu Ser Asp Arg Glu Thr Leu Ala
228                 165                 170                 175
229  Ala Ser Met Gln Thr Ile Leu Asp Glu Ala Thr Glu Ser Trp Gly Ile
230                 180                 185                 190
231  Lys Val Glu Arg Val Glu Ile Lys Asp Val Arg Leu Pro Ile Gln Leu
232            195                 200                 205
233  Gln Arg Ala Met Ala Ala Glu Ala Glu Ala Thr Arg Glu Ala Arg Ala
234       210                 215                 220
235  Lys Val Ile Ala Ala Glu Gly Glu Gln Lys Ala Ser Arg Ala Leu Arg
236  225                 230                 235                 240
237  Asp Ala Ala Ser Val Ile Ala Gln Ser Pro Ala Ala Leu Gln Leu Arg
238                 245                 250                 255
239  Tyr Leu Gln Thr Leu Asn Ser Val Ala Arg Glu Lys Phe Asp Asp His
240                 260                 265                 270
241  Leu Pro Thr Ser Asp Gly Ile Ser
242            275                 280
244  (2) INFORMATION FOR SEQ ID NO: 5:
246       (i) SEQUENCE CHARACTERISTICS:
247            (A) LENGTH: 415 amino acids
248            (B) TYPE: amino acid
249            (C) STRANDEDNESS: single
250            (D) TOPOLOGY: linear
252     (vii) IMMEDIATE SOURCE:
253            (A) LIBRARY: GenBank
254            (B) CLONE: 1353669
256      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
258  Met Glu Tyr Gly Met Pro Glu Gly Ser Tyr Asp Ser Val Phe Thr Tyr
259   1               5                 10                 15
260  Ala Pro Tyr Asn Asp Leu Asp Lys Met Gly Tyr Met Gly Pro Ala Arg
261            20                 25                 30
262  Gln Gly Met Met Leu Gly Asn Lys Tyr Gly Asn Phe Thr Tyr Thr Arg
263            35                 40                 45
264  Asp Tyr Gly Val Asn Met Glu Asp Asp Ile Lys Pro Leu Ser Ala Ile
265       50                 55                 60
266  Glu Leu Leu Ile Phe Cys Val Ser Phe Leu Phe Val Val Met Thr Met
267  65               70                 75                 80
268  Pro Leu Ser Leu Leu Phe Ala Leu Lys Phe Ile Ser Thr Ser Glu Lys
269                 85                 90                 95
270  Leu Val Val Leu Arg Leu Gly Arg Ala Gln Lys Thr Arg Gly Pro Gly
271            100                105                 110
272  Ile Thr Leu Val Ile Pro Cys Ile Asp Thr Thr His Lys Val Thr Met
273            115                120                 125
274  Ser Ile Thr Ala Phe Asn Val Pro Pro Leu Gln Ile Ile Thr Thr Asp
275       130                 135                 140
```

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**VERIFICATION SUMMARY**          DATE: 01/25/2002
PATENT APPLICATION:   US/09/898,216          TIME: 16:58:05

Input Set : **N:\Crf3\RULE60\09898216.raw**
Output Set: **N:\CRF3\01252002\I898216.raw**

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1